

SEQUENCE LISTING

<110> Sprecher, Cindy A.
Novak, Julia E.
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Presnell, Scott R.
Holly, Richard D.
Nelson, Andrew J.

<120> SOLUBLE ZALPHA11 CYTOKINE RECEPTORS

<130> 00-22

<150> US 60/194,731
<151> 2000-04-05

<150> US 60/222,121
<151> 2000-07-28

<160> 86

<170> FastSEQ for Windows Version 3.0

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<212> DNA
<213> Homo sapiens

<220>
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ggc tgg ggc tgc ccc gac ctc gtc tac acc gat tac ctc cag acg 96
Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
20 25 30

gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc 144

Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr			
35	40	45	
ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc			192
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser			
50	55	60	
tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc			240
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr			
65	70	75	80
tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc			288
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val			
85	90	95	
aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt			336
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe			
100	105	110	
ctc ctg gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg			384
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val			
115	120	125	
acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac			432
Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp			
130	135	140	
cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac			480
Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr			
145	150	155	160
agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc			528
Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile			
165	170	175	
tca gtg gac tca aga agt gtc tcc ctc ccc ctg gag ttc cgc aaa			576
Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys			
180	185	190	
gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc			624
Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser			
195	200	205	

tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln	672
210 215 220	
acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu	720
225 230 235 240	
ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys	768
245 250 255	
acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser	816
260 265 270	
cct gag cggttccatgcccctgtac aag ggc tgc agc gga gac ttc Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe	864
275 280 285	
aag aaa ttgggttggttgc ccc ttc act ggc tcc agc ctg gag ctg gga Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly	912
290 295 300	
ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His	960
305 310 315 320	
cca cca cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu	1008
325 330 335	
cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp	1056
340 345 350	
ccg aca gcc cag aac tcg ggg ggc tca gct tac agt gag gag agg gat Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp	1104
355 360 365	
ccg cca tac ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala	1152
370 375 380	

gag ggg cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro 385 390 395 400	1200
gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp 405 410 415	1248
cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser 420 425 430	1296
gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg 435 440 445	1344
cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro 450 455 460	1392
tgg ggt ggc cg ^g tca cct gga ggg gtc tca gag agt gag gcg ggc tca Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser 465 470 475 480	1440
ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly 485 490 495	1488
tct gac tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp 500 505 510	1536
gaa gga ccc ccc cg ^g agc tac ctc cgc cag tgg gtg gtc att cct ccg Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro 515 520 525	1584
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<212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50 55 60
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65 70 75 80
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85 90 95
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 115 120 125
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 180 185 190
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
 225 230 235 240
 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
 245 250 255
 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
 260 265 270
 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
 275 280 285
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
 290 295 300

Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
 305 310 315 320
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 325 330 335
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 340 345 350
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 355 360 365
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 370 375 380
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 385 390 395 400
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 405 410 415
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 420 425 430
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 435 440 445
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 450 455 460
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
 465 470 475 480
 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
 485 490 495
 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
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 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
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 <213> Homo sapiens

<220>
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gat ttc ttc ctg acc act atg ccc act gac tcc ctc agt gtt tcc act				96
Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser Leu Ser Val Ser Thr				
20	25	30		
ctg ccc ctc cca gag gtt cag tgt ttt gtg ttc aat gtc gag tac atg				144
Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met				
35	40	45		
aat tgc act tgg aac agc agc tct gag ccc cag cct acc aac ctc act				192
Asn Cys Thr Trp Asn Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr				
50	55	60		
ctg cat tat tgg tac aag aac tcg gat aat gat aaa gtc cag aag tgc				240
Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys				
65	70	75	80	
agc cac tat cta ttc tct gaa gaa atc act tct ggc tgt cag ttg caa				288
Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln				
85	90	95		
aaa aag gag atc cac ctc tac caa aca ttt gtt gtt cag ctc cag gac				336
Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp				
100	105	110		
cca cgg gaa ccc agg aga cag gcc aca cag atg cta aaa ctg cag aat				384
Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn				
115	120	125		
ctg gtg atc ccc tgg gct cca gag aac cta aca ctt cac aaa ctg agt				432
Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser				
130	135	140		
gaa tcc cag cta gaa ctg aac tgg aac aac aga ttc ttg aac cac tgt				480
Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys				
145	150	155	160	
ttg gag cac ttg gtg cag tac cgg act gac tgg gac cac agc tgg act				528
Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr				
165	170	175		

gaa caa tca gtg gat tat aga cat aag ttc tcc ttg cct agt gtg gat Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp	180	185	190	576
ggg cag aaa cgc tac acg ttt cgt gtt cg ^g agc cgc ttt aac cca ctc Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu	195	200	205	624
tgt gga agt gct cag cat tgg agt gaa tgg agc cac cca atc cac tgg Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp	210	215	220	672
ggg agc aat act tca aaa gag aat Gly Ser Asn Thr Ser Lys Glu Asn	225	230		696
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Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met				
35	40	45		
Asn Cys Thr Trp Asn Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr				
50	55	60		
Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys				
65	70	75	80	
Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln				
85	90	95		
Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp				
100	105	110		
Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn				
115	120	125		
Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser				
130	135	140		
Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys				
145	150	155	160	

Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
 165 170 175
 Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
 180 185 190
 Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu
 195 200 205
 Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp
 210 215 220
 Gly Ser Asn Thr Ser Lys Glu Asn
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 <213> Homo sapiens

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caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu 35 40 45	144
cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met 50 55 60	192
gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr 65 70 75 80	240
gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct	288

Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala			
85	90	95	
gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg acc ttc tca			336
Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser			
100	105	110	
gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc			384
Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe			
115	120	125	
tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac ccg			432
Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg			
130	135	140	
gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg gac			480
Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp			
145	150	155	160
tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa gac tcg agc			528
Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser			
165	170	175	
tat gag ctg cag gtg cg gca ggg ccc atg cct ggc tcc tcc tac cag			576
Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln			
180	185	190	
ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cac tca			624
Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser			
195	200	205	
gag gag tta aag gaa ggc tgg aac cct cac			654
Glu Glu Leu Lys Glu Gly Trp Asn Pro His			
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 20 25 30
 Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu
 35 40 45
 His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
 50 55 60
 Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
 65 70 75 80
 Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala
 85 90 95
 Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser
 100 105 110
 Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe
 115 120 125
 Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg
 130 135 140
 Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp
 145 150 155 160
 Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser
 165 170 175
 Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln
 180 185 190
 Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser
 195 200 205
 Glu Glu Leu Lys Glu Gly Trp Asn Pro His
 210 215

<210> 7

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of soluble
 zalpha1 Receptor polypeptide as shown in SEQ ID
 NO:6

<221> misc_feature

<222> (1)...(654)

<223> n = A,T,C or G

<400> 7

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gaygargcna	cnwsntgyws	nytncaymgn	wsngcncaya	aygcnacnca	ygcnacntay	180
acntgycaya	tggaygtntt	ycayttyatg	gcnaygaya	thtysngt	naayathacn	240
gaycarwsng	gnaaytayws	ncargartgy	ggnwsnttly	tntngcnga	rwsnathaar	300
ccngcncnc	cntyaygt	nacngtnacn	ttywsnggnc	artayaayat	hwsntggmgn	360
wsngaytayg	argayccngc	nttytayatg	ytnaarggna	arytnccarta	ygarytnkar	420
taymgnaaym	gnngngaycc	ntggcngtn	wsnccnmgnm	gnaarytnat	hwsngtngay	480
wsnmgnwsng	tnwsnytnyt	nccnytngar	ttymgnarg	aywsnwsnta	ygarytnkar	540
gtnmgnngcng	gnccnatgcc	nggnwsnwsn	taycarggna	cntggwsnga	rtggwsngay	600
ccngtnatht	tycaracnca	rwsngargar	ytnaargarg	gntgaaaycc	ncay	654

<210> 8

<211> 696

<212> DNA

<213> Artificial Sequence

<220>

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<221> misc_feature

<222> (1)...(696)

<223> n = A,T,C or G

<400> 8

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ttygtnttya	aygtngarta	yatgaaytgy	acntggayw	snwsnwsnga	rccncarccn	180
acnaayytna	cnytnayta	ytggtayaar	aaywsngaya	aygayaargt	ncaraartgy	240
wsncaytayy	tnttysnsga	rgarathacn	wsngngtgc	arytnccaraa	raargarath	300
cayytntayc	aracnttygt	ngtncarytn	cargayccnm	ngarccnm	nmgnrcargcn	360
acncaratgy	tnaarytnca	raaytngtn	athccntgg	cnccngaraa	ytnacnytn	420
cayaarytnw	sngarwsnca	rytngarytn	aaytggayaa	aymgnatty	naaycaytgy	480
ytngrcayy	tngtncarta	ymgnacngay	tggaycaww	sntggacnga	rcarwsngtn	540
gaytaymgnc	ayaarttyws	nytnccnwsn	gtngayggnc	araarmnta	yacnttymgn	600
gtnmgnwsnm	gnttayaaycc	nytnctgyggn	wsngcncarc	aytggwsnga	rtggwsncay	660
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<211> 486

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(486)

<400> 9

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1				5						10					15		
gtc	atc	ttc	ttg	ggg	aca	ctg	gtc	cac	aaa	tca	agc	tcc	caa	ggt	caa		96
Val	Ile	Phe	Leu	Gly	Thr	Leu	Val	His	Lys	Ser	Ser	Ser	Gln	Gly	Gln		
					20					25					30		
gat	cgc	cac	atg	att	aga	atg	cgt	caa	ctt	ata	gat	att	gtt	gat	cag		144
Asp	Arg	His	Met	Ile	Arg	Met	Arg	Gln	Leu	Ile	Asp	Ile	Val	Asp	Gln		
					35					40					45		
ctg	aaa	aat	tat	gtg	aat	gac	ttg	gtc	cct	gaa	ttt	ctg	cca	gct	cca		192
Leu	Lys	Asn	Tyr	Val	Asn	Asp	Leu	Val	Pro	Glu	Phe	Leu	Pro	Ala	Pro		
					50					55					60		
gaa	gat	gta	gag	aca	aac	tgt	gag	tgg	tca	gct	ttt	tcc	tgt	ttt	cag		240
Glu	Asp	Val	Glu	Thr	Asn	Cys	Glu	Trp	Ser	Ala	Phe	Ser	Cys	Phe	Gln		
					65					70					75		80
aag	gcc	caa	cta	aag	tca	gca	aat	aca	gga	aac	aat	gaa	agg	ata	atc		288
Lys	Ala	Gln	Leu	Lys	Ser	Ala	Asn	Thr	Gly	Asn	Asn	Glu	Arg	Ile	Ile		
						85					90				95		
aat	gta	tca	att	aaa	aag	ctg	aag	agg	aaa	cca	cct	tcc	aca	aat	gca		336
Asn	Val	Ser	Ile	Lys	Lys	Leu	Lys	Arg	Lys	Pro	Pro	Ser	Thr	Asn	Ala		
						100				105					110		
ggg	aga	aga	cag	aaa	cac	aga	cta	aca	tgc	cct	tca	tgt	gat	tct	tat		384
Gly	Arg	Arg	Gln	Lys	His	Arg	Leu	Thr	Cys	Pro	Ser	Cys	Asp	Ser	Tyr		
						115				120					125		
gag	aaa	aaa	cca	ccc	aaa	gaa	ttc	cta	gaa	aga	ttc	aaa	tca	ctt	ctc		432
Glu	Lys	Lys	Pro	Pro	Lys	Glu	Phe	Leu	Glu	Arg	Phe	Lys	Ser	Leu	Leu		
						130				135					140		

caa aag atg att cat cag cat ctg tcc tct aga aca cac gga agt gaa 480
 Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu
 145 150 155 160

gat tcc 486
Asp Ser

<210> 10
<211> 162
<212> PRT
<213> *Homo sapiens*

<400>	10		
Met Arg Ser Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met			
1	5	10	15
Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln			
20	25	30	
Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln			
35	40	45	
Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro			
50	55	60	
Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln			
65	70	75	80
Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile			
85	90	95	
Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala			
100	105	110	
Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr			
115	120	125	
Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu			
130	135	140	
Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu			
145	150	155	160
Asp Ser			

<210> 11
<211> 1735
<212> DNA
<213> mus musculus

<220>
<221> CDS

<222> (143)...(1729)

<400> 11

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cggccaggag accacccaag tgccccagcc taaagaatgg ctttctgaga aagaccctga	120
aggagtaggt ctggacaca gc atg ccc cg ggc cca gtg gct gcc tta ctc	172
Met Pro Arg Gly Pro Val Ala Ala Leu Leu	
1 5 10	
ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act tgc tac	220
Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr	
15 20 25	
act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg agc ccc	268
Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg Ser Pro	
30 35 40	
aac ccc agc ata ctc agt ctc acc tgg caa gat gaa tat gag gaa ctt	316
Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu	
45 50 55	
cag gac caa gag acc ttc tgc agc cta cac agg tct ggc cac aac acc	364
Gln Asp Gln Glu Thr Phe Cys Ser Leu His Arg Ser Gly His Asn Thr	
60 65 70	
aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc ctg tcc	412
Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe Leu Ser	
75 80 85 90	
gat gaa gtt ttc att gtc aat gtg acg gac cag tct ggc aac aac tcc	460
Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn Asn Ser	
95 100 105	
caa gag tgt ggc agc ttt gtc ctg gct gag agc atc aaa cca gct ccc	508
Gln Glu Cys Gly Ser Phe Val Leu Ala Glu Ser Ile Lys Pro Ala Pro	
110 115 120	
ccc ttg aac gtg act gtg gcc ttc tca gga cgc tat gat atc tcc tgg	556
Pro Leu Asn Val Thr Val Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp	
125 130 135	
gac tca gct tat gac gaa ccc tcc aac tac gtg ctg agg ggc aag cta	604

Asp Ser Ala Tyr Asp Glu Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu			
140	145	150	
caa tat gag ctg cag tat cgg aac ctc aga gac ccc tat gct gtg agg			652
Gln Tyr Glu Leu Gln Tyr Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg			
155	160	165	170
ccg gtg acc aag ctg atc tca gtg gac tca aga aac gtc tct ctt ctc			700
Pro Val Thr Lys Leu Ile Ser Val Asp Ser Arg Asn Val Ser Leu Leu			
175	180	185	
cct gaa gag ttc cac aaa gat tct agc tac cag ctg cag gtg cggt gca			748
Pro Glu Glu Phe His Lys Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala			
190	195	200	
gcg cct cag cca ggc act tca ttc agg ggg acc tgg agt gag tgg agt			796
Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser			
205	210	215	
gac ccc gtc atc ttt cag acc cag gct ggg gag ccc gag gca ggc tgg			844
Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp			
220	225	230	
gac cct cac atg ctg ctg ctc ctg gct gtc ttg atc att gtc ctg gtt			892
Asp Pro His Met Leu Leu Leu Ala Val Leu Ile Ile Val Leu Val Val			
235	240	245	250
ttc atg ggt ctg aag atc cac ctg cct tgg agg cta tgg aaa aag ata			940
Phe Met Gly Leu Lys Ile His Leu Pro Trp Arg Leu Trp Lys Lys Ile			
255	260	265	
tgg gca cca gtg ccc acc cct gag agt ttc ttc cag ccc ctg tac agg			988
Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg			
270	275	280	
gag cac agc ggg aac ttc aag aaa tgg gtt aat acc cct ttc acg gcc			1036
Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe Thr Ala			
285	290	295	
tcc agc ata gag ttg gtg cca cag agt tcc aca aca aca tca gcc tta			1084
Ser Ser Ile Glu Leu Val Pro Gln Ser Ser Thr Thr Ser Ala Leu			
300	305	310	

cat ctg tca ttg tat cca gcc aag gag aag aag ttc ccg ggg ctg ccg His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro 315 320 325 330	1132
ggt ctg gaa gag caa ctg gag tgt gat gga atg tct gag cct ggt cac Gly Leu Glu Glu Gln Leu Glu Cys Asp Gly Met Ser Glu Pro Gly His 335 340 345	1180
tgg tgc ata atc ccc ttg gca gct ggc caa gcg gtc tca gcc tac agt Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser 350 355 360	1228
gag gag aga gac cg ^g cca tat ggt ctg gtg tcc att gac aca gtg act Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr 365 370 375	1276
gtg gga gat gca gag ggc ctg tgt gtc tgg ccc tgt agc tgt gag gat Val Gly Asp Ala Glu Gly Leu Cys Val Trp Pro Cys Ser Cys Glu Asp 380 385 390	1324
gat ggc tat cca gcc atg aac ctg gat gct ggc cga gag tct ggc cct Asp Gly Tyr Pro Ala Met Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro 395 400 405 410	1372
aat tca gag gat ctg ctc ttg gtc aca gac cct gct ttt ctg tct tgc Asn Ser Glu Asp Leu Leu Leu Val Thr Asp Pro Ala Phe Leu Ser Cys 415 420 425	1420
ggc tgt gtc tca ggt agt ggt ctc agg ctt gga ggc tcc cca ggc agc Gly Cys Val Ser Gly Ser Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser 430 435 440	1468
cta ctg gac agg ttg agg ctg tca ttt gca aag gaa ggg gac tgg aca Leu Leu Asp Arg Leu Arg Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr 445 450 455	1516
gca gac cca acc tgg aga act ggg tcc cca gga ggg ggc tct gag agt Ala Asp Pro Thr Trp Arg Thr Gly Ser Pro Gly Gly Ser Glu Ser 460 465 470	1564
gaa gca ggt tcc ccc cct ggt ctg gac atg gac aca ttt gac agt ggc	1612

Glu Ala Gly Ser Pro Pro Gly Leu Asp Met Asp Thr Phe Asp Ser Gly				
475	480	485	490	
ttt gca ggt tca gac tgt ggc agc ccc gtg gag act gat gaa gga ccc				1660
Phe Ala Gly Ser Asp Cys Gly Ser Pro Val Glu Thr Asp Glu Gly Pro				
495	500	505		
cct cga agc tat ctc cgc cag tgg gtg gtc agg acc cct cca cct gtg				1708
Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Arg Thr Pro Pro Pro Val				
510	515	520		
gac agt gga gcc cag agc agc tagcat				1735
Asp Ser Gly Ala Gln Ser Ser				
525				
<210> 12				
<211> 529				
<212> PRT				
<213> mus musculus				
<400> 12				
Met Pro Arg Gly Pro Val Ala Ala Leu Leu Leu Ile Leu His Gly				
1	5	10	15	
Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr				
20	25	30		
Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser				
35	40	45		
Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe				
50	55	60		
Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr				
65	70	75	80	
Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val				
85	90	95		
Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe				
100	105	110		
Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val				
115	120	125		
Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu				
130	135	140		
Pro Ser Asn Tyr Val Leu Arg Gln Lys Leu Gln Tyr Glu Leu Gln Tyr				
145	150	155	160	

Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys
 180 185 190
 Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala Ala Pro Gln Pro Gly Thr
 195 200 205
 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Met Leu Leu
 225 230 235 240
 Leu Leu Ala Val Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile
 245 250 255
 His Leu Pro Trp Arg Leu Trp Lys Lys Ile Trp Ala Pro Val Pro Thr
 260 265 270
 Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg Glu His Ser Gly Asn Phe
 275 280 285
 Lys Lys Trp Val Asn Thr Pro Phe Thr Ala Ser Ser Ile Glu Leu Val
 290 295 300
 Pro Gln Ser Ser Thr Thr Ser Ala Leu His Leu Ser Leu Tyr Pro
 305 310 315 320
 Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro Gly Leu Glu Glu Gln Leu
 325 330 335
 Glu Cys Asp Gly Met Ser Glu Pro Gly His Trp Cys Ile Ile Pro Leu
 340 345 350
 Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro
 355 360 365
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Gly Asp Ala Glu Gly
 370 375 380
 Leu Cys Val Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Met
 385 390 395 400
 Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro Asn Ser Glu Asp Leu Leu
 405 410 415
 Leu Val Thr Asp Pro Ala Phe Leu Ser Cys Gly Cys Val Ser Gly Ser
 420 425 430
 Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser Leu Leu Asp Arg Leu Arg
 435 440 445
 Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr Ala Asp Pro Thr Trp Arg
 450 455 460
 Thr Gly Ser Pro Gly Gly Ser Glu Ser Glu Ala Gly Ser Pro Pro
 465 470 475 480
 Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Ala Gly Ser Asp Cys
 485 490 495

Gly Ser Pro Val Glu Thr Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg
 500 505 510
 Gln Trp Val Val Arg Thr Pro Pro Pro Val Asp Ser Gly Ala Gln Ser
 515 520 525
 Ser

<210> 13
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> WSXWS polypeptide consensus motif

<221> VARIANT
 <222> (1)...(5)
 <223> Xaa = Any Amino Acid

<400> 13
 Trp Ser Xaa Trp Ser
 1 5

<210> 14
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Glu-Glu (CEE) Tag amino acid sequence

<400> 14
 Glu Tyr Met Pro Met Glu
 1 5

<210> 15
 <211> 1701
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> soluble zalpha1R/IgGgamma1 construct

<221> CDS

<222> (1)...(1701)

<400> 15

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1 5 10 15	
ggc tgg ggc tgc ccc gac ctc gtc tac acc gat tac ctc cag acg Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr	96
20 25 30	
gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr	144
35 40 45	
ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser	192
50 55 60	
tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr	240
65 70 75 80	
tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val	288
85 90 95	
aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe	336
100 105 110	
ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val	384
115 120 125	
acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp	432
130 135 140	
cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr	480
145 150 155 160	

agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile 165	170	175	528
tca gtg gac tca aga agt gtc tcc ctc ccc ctg gag ttc cgc aaa Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys 180	185	190	576
gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser 195	200	205	624
tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln 210	215	220	672
acc cag tca gag gag tta aag gaa ggc tgg aac cct cac gct agc acc Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Ala Ser Thr 225	230	235	720
aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser 245	250	255	768
ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu 260	265	270	816
ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His 275	280	285	864
acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser 290	295	300	912
gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys 305	310	315	960
aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag			1008

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu			
325	330	335	
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct			1056
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro			
340	345	350	
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag			1104
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys			
355	360	365	
gac acc ctc atg atc tcc ccg acc cct gag gtc aca tgc gtg gtg gtg			1152
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val			
370	375	380	
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac			1200
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp			
385	390	395	400
ggc gtg gag gtg cat aat gcc aag aca aag ccg ccg gag gag cag tac			1248
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr			
405	410	415	
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac			1296
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp			
420	425	430	
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc			1344
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu			
435	440	445	
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga			1392
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg			
450	455	460	
gaa cca cag gtg tac acc ctg ccc cca tcc ccg gat gag ctg acc aag			1440
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys			
465	470	475	480
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac			1488
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp			
485	490	495	

atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 500 505 510	1536
acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 515 520 525	1584
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser 530 535 540	1632
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 545 550 555 560	1680
ctc tcc ctg tct ccg ggt aaa Leu Ser Leu Ser Pro Gly Lys 565	1701
<210> 16	
<211> 567	
<212> PRT	
<213> Artificial Sequence	
<400> 16	
Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly 1 5 10 15	
Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr 20 25 30	
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr 35 40 45	
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser 50 55 60	
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr 65 70 75 80	
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val 85 90 95	
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe 100 105 110	
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val 115 120 125	

Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 180 185 190
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Ala Ser Thr
 225 230 235 240
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 245 250 255
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 260 265 270
 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 275 280 285
 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 290 295 300
 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 305 310 315 320
 Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 325 330 335
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 340 345 350
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 355 360 365
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 370 375 380
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 385 390 395 400
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 405 410 415
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 420 425 430
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 435 440 445
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 465 470 475 480
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 485 490 495
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 500 505 510
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 515 520 525
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 530 535 540
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 545 550 555 560
 Leu Ser Leu Ser Pro Gly Lys
 565

<210> 17
 <211> 1083
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> soluble human IL-2Rgamma/human kappa light chain
 construct

<221> CDS
 <222> (1)...(1083)

<400> 17

atg ttg aag cca tca tta cca ttc aca tcc ctc tta ttc ctg cag ctg	48
Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu	
1 5 10 15	

ccc ctg ctg gga gtg ggg ctg aac acg aca att ctg acg ccc aat ggg 96
 Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
 20 25 30

aat gaa gac acc aca gct gat ttc ttc ctg acc act atg ccc act gac 144
 Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
 35 40 45

tcc ctc agt gtt tcc act ctg ccc ctc cca gag gtt cag tgt ttt gtg 192

Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val	
50						55				60						
ttc	aat	gtc	gag	tac	atg	aat	tgc	act	tgg	aac	agc	agc	tct	gag	ccc	240
Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro	
65						70				75				80		
cag	cct	acc	aac	ctc	act	ctg	cat	tat	tgg	tac	aag	aac	tcg	gat	aat	288
Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn	
						85				90			95			
gat	aaa	gtc	cag	aag	tgc	agc	cac	tat	cta	ttc	tct	gaa	gaa	atc	act	336
Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr	
						100			105			110				
tct	ggc	tgt	cag	ttg	caa	aaa	aag	gag	atc	cac	ctc	tac	caa	aca	ttt	384
Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe	
						115			120			125				
gtt	gtt	cag	ctc	cag	gac	cca	cg	gaa	ccc	agg	aga	cag	gcc	aca	cag	432
Val	Val	Gln	Leu	Gln	Asp	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln	
						130			135			140				
atg	cta	aaa	ctg	cag	aat	ctg	gtg	atc	ccc	tgg	gct	cca	gag	aac	cta	480
Met	Leu	Lys	Leu	Gln	Asn	Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu	
						145			150			155			160	
aca	ctt	cac	aaa	ctg	agt	gaa	tcc	cag	cta	gaa	ctg	aac	tgg	aac	aac	528
Thr	Leu	His	Lys	Leu	Ser	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn	
						165			170			175				
aga	ttc	ttg	aac	cac	tgt	ttg	gag	cac	ttg	gtg	cag	tac	cg	act	gac	576
Arg	Phe	Leu	Asn	His	Cys	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp	
						180			185			190				
tgg	gac	cac	agc	tgg	act	gaa	caa	tca	gtg	gat	tat	aga	cat	aag	ttc	624
Trp	Asp	His	Ser	Trp	Thr	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe	
						195			200			205				
tcc	ttg	cct	agt	gtg	gat	ggg	cag	aaa	cgc	tac	acg	ttt	cgt	gtt	cg	672
Ser	Leu	Pro	Ser	Val	Asp	Gly	Gln	Lys	Arg	Tyr	Thr	Phe	Arg	Val	Arg	
						210			215			220				

agc cgc ttt aac cca ctc tgt gga agt gct cag cat tgg agt gaa tgg			720
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp			
225	230	235	240
agc cac cca atc cac tgg ggg agc aat act tca aaa gag aat act gtg			768
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Thr Val			
245	250	255	
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa			816
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys			
260	265	270	
tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga			864
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg			
275	280	285	
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac			912
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn			
290	295	300	
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc			960
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser			
305	310	315	320
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa			1008
Leu Ser Ser Thr Leu Thr Ser Lys Ala Asp Tyr Glu Lys His Lys			
325	330	335	
gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca			1056
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr			
340	345	350	
aag agc ttc aac agg gga gag tgt tag			1083
Lys Ser Phe Asn Arg Gly Glu Cys *			
355	360		
<210> 18			
<211> 360			
<212> PRT			
<213> Artificial Sequence			

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 Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1 5 10 15
 Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
 20 25 30
 Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
 35 40 45
 Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
 50 55 60
 Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
 65 70 75 80
 Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
 85 90 95
 Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
 100 105 110
 Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
 115 120 125
 Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
 130 135 140
 Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
 145 150 155 160
 Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
 165 170 175
 Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
 180 185 190
 Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
 195 200 205
 Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
 210 215 220
 Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
 225 230 235 240
 Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Thr Val
 245 250 255
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 260 265 270
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 275 280 285
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 290 295 300
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 305 310 315 320

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 325 330 335
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 340 345 350
 Lys Ser Phe Asn Arg Gly Glu Cys
 355 360

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 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC19905

<400> 19

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<220>
 <223> Oligonucleotide primer ZC19906

<400> 20

acagaattct tagctggcct ggggtccagg cgt 33

<210> 21
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC19931

<400> 21

ggttggtacc gcaagatgcc gcgtggctgg gccgcc 36

<210> 22
 <211> 29

<212> DNA		
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<220>		
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<400> 22		
cgaggatcc gtgagggttc cagccttcc		29
<210> 23		
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<212> PRT		
<213> Artificial Sequence		
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<223> FLAG tag amino acid sequence		
<400> 23		
Asp Tyr Lys Asp Asp Asp Asp Lys		
1	5	.
<210> 24		
<211> 66		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Oligonucleotide primer spanning vector flanking		
region and the 5' end of the zalpha1		
<400> 24		
tccactttgc ctttctctcc acaggtgtcc aggaaattca tcgataatgc cgctggctg		60
ggccgc		66
<210> 25		
<211> 699		
<212> DNA		
<213> Homo sapiens		
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gagcccagat cttcagacaa aactcacaca tgccccaccgt gcccagcacc tgaagccgag		60
ggggcaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccg		120
acccctgagg tcacatgcgt ggtggtgac gtgagccacg aagaccctga ggtcaagttc		180

aactggta	cg tggacggcgt ggagg	tgcat aatgccaaga caaagccgcg ggagg	ggcag	240
tacaacagca	cgtaccgtgt ggtcagcgtc	ctcaccgtcc tg	caccagga ctggctgaat	300
ggcaaggagt	acaagtgc	aaagccctcc catcctccat cgagaaaacc		360
atctccaaag	ccaaagggca	gccccc gagaa ccacaggtgt acacc	ctgccc	420
gatgagctga	ccaagaacca	ggtcagcctg acc	tcgtt ctatccc	480
gacatcgccg	tggagtgg	gagcaatggg cagccggaga acaactaca	gaccacgc	540
cccgtctgg	actccgacgg	ctc	ttcacagca agtcaccgt ggacaagagc	600
aggtggc	agggaacgt	tttctcatgc tc	cgatgc atgaggctct gcacaaccac	660
tacacgcaga	agacgc	tc	gtctccg gttaaataaa	699
<210>	26			
<211>	62			
<212>	DNA			
<213>	Artificial Sequence			
<220>				
<223>	First Oligonucleotide primer spanning 3' end of			
	the zalpha1 extracellular domain and the 5' end			
	of Fc4			
<400>	26			
gcacgg	ttgg catgtgtgag ttttgtctga agatctggc tcgtgagg	gt tccagc	c	60
ct				62
<210>	27			
<211>	61			
<212>	DNA			
<213>	Artificial Sequence			
<220>				
<223>	Second Oligonucleotide primer spanning 3' end of			
	the zalpha1 extracellular domain and the 5' end			
	of Fc4			
<400>	27			
agacccagtc	agaggagtta aaggaaggct ggaaccctca cgagcccaga	tcttc	agaca	60
a				61
<210>	28			
<211>	67			
<212>	DNA			
<213>	Artificial Sequence			

<220>

<223> Oligonucleotide primer spanning the 3' end of Fc4 and the vector flanking region

<400> 28

gtgggcctct ggggtggta caacccaga gctgtttaa tctagattat ttacccggag 60
acaggqa 67

<210> 29

<211> 1821

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide encoding MBP-human zalpha1I soluble receptor fusion

<221> CDS

<??> (1)...(1821)

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1 5 10 15

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc 96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc 144
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

cca cag gtt gct gca act ggc gat ggc cct gac att atc ttc tgg gca 192
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
65 70 75 80

acc ccq qac aaa qcq ttc caq qac aaq ctq tat ccq ttt acc tqq qat 288

Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp			
85	90	95	
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa			336
Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu			
100	105	110	
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa			384
Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys			
115	120	125	
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt			432
Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly			
130	135	140	
aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg			480
Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro			
145	150	155	160
ctg att gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag			528
Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys			
165	170	175	
tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt			576
Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly			
180	185	190	
ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac			624
Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp			
195	200	205	
acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg			672
Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Glu Thr Ala			
210	215	220	
atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa			720
Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys			
225	230	235	240
gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc			768
Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser			
245	250	255	

aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln 325 330 335	1008
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala 340 345 350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn 355 360 365	1104
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val 370 375 380	1152
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln 385 390 395 400	1200
acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu 405 410 415	1248
acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc	1296

Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr			
420	425	430	
tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac			1344
Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr			
435	440	445	
acc tgc cac atg gta ttc cac ttc atg gcc gac gac att ttc agt			1392
Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser			
450	455	460	
gtc aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc			1440
Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser			
465	470	475	480
ttt ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act			1488
Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr			
485	490	495	
gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa			1536
Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu			
500	505	510	
gac cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag			1584
Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln			
515	520	525	
tac agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg			1632
Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu			
530	535	540	
atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc			1680
Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg			
545	550	555	560
aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc			1728
Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly			
565	570	575	
tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt			1776
Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe			
580	585	590	

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 Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His *
 595 600 605

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<211> 606
<212> PRT
<213> Artificial Sequence

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 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val
 370 375 380
 Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln
 385 390 395 400
 Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu
 405 410 415
 Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr
 420 425 430
 Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr
 435 440 445
 Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser
 450 455 460
 Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser
 465 470 475 480
 Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr
 485 490 495
 Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu
 500 505 510
 Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln
 515 520 525
 Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu
 530 535 540
 Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg
 545 550 555 560
 Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly
 565 570 575
 Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe
 580 585 590

Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His
 595 600 605

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gacgaggcca	cctcctgcag	cctccacagg	tcggcccaca	atgccacgca	tgccacctac	180
acctgcccaca	tggatgtatt	ccacttcatg	gccgacgaca	ttttcagtgt	caacatcaca	240
gaccagtctg	gcaactactc	ccaggagtgt	ggcagcttc	tcctggctga	gagcatcaag	300
ccggctcccc	cttcaacgt	gactgtgacc	ttctcaggac	agtataatat	ctcctggcgc	360
tcagattacg	aagaccctgc	tttctacatg	ctgaagggca	agcttcagta	tgagctgcag	420
tacaggaacc	ggggagaccc	ctgggctgtg	agtccgagga	gaaagctgat	ctcagtgac	480
tcaagaagtg	tctccctcct	ccccctggag	ttccgcaaag	actcgagcta	tgagctgcag	540
gtgcggccag	ggcccatgcc	tggctctcc	taccagggga	cctggagtga	atggagtgac	600
ccggtcatct	ttcagaccca	gtcagaggag	ttaaaggaag	gctggAACCC	tcactag	657

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 <211> 65
 <212> DNA
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<220>
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caccg						65

<210> 33
 <211> 68
 <212> DNA
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<220>
 <223> Oligonucleotide primerZC20185

<400> 33

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<210> 34	
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<210> 36	
<211> 60	
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<213> Artificial Sequence	
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<223> Oligonucleotide primerZC19352	
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<210> 37	
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<223> Oligonucleotide primer ZC22276
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gcttgcctt cagcatgtag a 21
<210> 42
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Zalpha11 TaqMan Probe, ZG31

<400> 42
cggctccccc tttcaacgtg act 23
<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer, rRNA forward primer

<400> 43
cggttaccac atccaaggaa 20
<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer, rRNA reverse primer

<400> 44
gctggaaattt ccgcggct 18
<210> 45
<211> 22
<212> DNA
<213> Artificial Sequence

<220>						
<223> rRNA TaqMan probe						
<400> 45						
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					1	
gag agg acc ctt gtc tgt ctg gta gtc atc ttc ttg ggg aca gtg gcc						104
Glu Arg Thr Leu Val Cys Leu Val Val Ile Phe Leu Gly Thr Val Ala						
5	10	15				
cat aaa tca agc ccc caa ggg cca gat cgc ctc ctg att aga ctt cgt						152
His Lys Ser Ser Pro Gln Gly Pro Asp Arg Leu Leu Ile Arg Leu Arg						
20	25	30				
cac ctt att gac att gtt gaa cag ctg aaa atc tat gaa aat gac ttg						200
His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu						
35	40	45				
gat cct gaa ctt cta tca gct cca caa gat gta aag ggg cac tgt gag						248
Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu						
50	55	60	65			
cat gca gct ttt gcc tgt ttt cag aag gcc aaa ctc aag cca tca aac						296
His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn						
70	75	80				
cct gga aac aat aag aca ttc atc att gac ctc gtg gcc cag ctc agg						344
Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg						
85	90	95				

agg agg ctg cct gcc agg agg gga gga aag aaa cag aag cac ata gct	392
Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala	
100 105 110	
aaa tgc cct tcc tgt gat tcg tat gag aaa agg aca ccc aaa gaa ttc	440
Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe	
115 120 125	
cta gaa aga cta aaa tgg ctc ctt caa aag atg att cat cag cat ctc	488
Leu Glu Arg Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His Leu	
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Ser	
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agactagtgt taactgttcc ccagaaaaatc gtcacaatca gaaccaacgc attctctttaa	1921
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gtctccatgt ttttatttctt tggtgttctt ggctgtgtaa ctgttgactt cttgacattt	2161

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gaataaaattt atagcattat tgatctatgt tattgctctg ttttattttac agtcacaccc 2941
gagaattttatg tttaatatac aatgtatgtac ttataactt aatgattttatt tattatgtat 3001
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<213> *Mus musculus*

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 20 25 30
 Arg His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp
 35 40 45
 Leu Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys
 50 55 60
 Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser
 65 70 75 80
 Asn Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu
 85 90 95
 Arg Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile
 100 105 110
 Ala Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu
 115 120 125
 Phe Leu Glu Arg Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His
 130 135 140
 Leu Ser
 145

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<220>
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cccacagtag gattctctt tgaagtattg	90	
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<211> 1707

<212> DNA

<213> homo sapiens

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gcc ctc gag ggg atg gag agg aag ctc tgc agt ccc aag cca ccc ccc	96
Ala Leu Glu Gly Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro	
20 25 30	

acc aag gcc tct ctc ccc act gac cct cca ggc tgg ggc tgc ccc gac	144
Thr Lys Ala Ser Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp	
35 40 45	

ctc gtc tac acc gat tac ctc cag acg gtc atc tgc atc ctg gaa	192
Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu	
50 55 60	

atg tgg aac ctc cac ccc agc acg ctc acc ctt acc tgg ata ctt tct	240
Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser	
65 70 75 80	

aat aat act ggg tgc tat atc aag gac aga aca ctg gac ctc agg caa	288
Asn Asn Thr Gly Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln	
85 90 95	

gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc cac	336
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Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His			
100	105	110	
agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg gat			384
Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp			
115	120	125	
gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca gac			432
Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp			
130	135	140	
cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct gag			480
Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu			
145	150	155	160
agc aga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc			528
Ser Arg Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala			
165	170	175	
ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac			576
Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn			
180	185	190	
cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg			624
Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val			
195	200	205	
gac tca aga agt gtc tcc ctc ccc ctg gag ttc cgc aaa gac tcg			672
Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser			
210	215	220	
agc tat gag ctg cag gtg cggt gca ggg ccc atg cct ggc tcc tcc tac			720
Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr			
225	230	235	240
cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag			768
Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln			
245	250	255	
tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt ctc ctc			816
Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu			
260	265	270	

ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag acc cat Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His 275 280 285	864
cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc cct gag Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu 290 295 300	912
cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc aag aaa Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys 305 310 315 320	960
tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga ccc tgg Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp 325 330 335	1008
agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac cca cca Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro 340 345 350	1056
cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa cca gca Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala 355 360 365	1104
gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg ccg aca Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr 370 375 380	1152
gcc cag aac tcg ggg ggc tca gct tac agt gag gag agg gat cgg cca Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro 385 390 395 400	1200
tac ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca gag ggg Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly 405 410 415	1248
cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca gcc ctg Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu 420 425 430	1296
gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac cca ctc Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu 435 440 445	1344

ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca gct ggc			1392
Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly			
450	455	460	
agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag			1440
Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys			
465	470	475	480
cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt			1488
Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly			
485	490	495	
ggc cg ^g tca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg			1536
Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu			
500	505	510	
gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac			1584
Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp			
515	520	525	
tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga			1632
Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly			
530	535	540	
ccc ccc cg ^g agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt			1680
Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu			
545	550	555	560
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Ser Ser Pro Gly Pro Gln Ala Ser *			
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20	25	30	

Thr Lys Ala Ser Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp
 35 40 45
 Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu
 50 55 60
 Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser
 65 70 75 80
 Asn Asn Thr Gly Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln
 85 90 95
 Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His
 100 105 110
 Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp
 115 120 125
 Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp
 130 135 140
 Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu
 145 150 155 160
 Ser Arg Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala
 165 170 175
 Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn
 180 185 190
 Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val
 195 200 205
 Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser
 210 215 220
 Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr
 225 230 235 240
 Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln
 245 250 255
 Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu
 260 265 270
 Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His
 275 280 285
 Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu
 290 295 300
 Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys
 305 310 315 320
 Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp
 325 330 335
 Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro
 340 345 350
 Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala
 355 360 365

Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr
 370 375 380
 Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro
 385 390 395 400
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly
 405 410 415
 Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu
 420 425 430
 Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu
 435 440 445
 Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly
 450 455 460
 Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys
 465 470 475 480
 Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly
 485 490 495
 Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu
 500 505 510
 Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp
 515 520 525
 Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly
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<211> 741

<212> DNA

<213> Artificial Sequence

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<221> misc_feature

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 ccnccnggnt ggggntgycc ngayyntgn tgytayacng aytayytnca racngtnath

60

120

tgyathyng aratgtggaa yytncayccn wsnaacnytna cnytnacntg gathytnwsn	180
aayaayacng gntgytat at haargaymgn acnytngayy tnmgnrcarga ycartaygar	240
garytnaarg aygargcnac nwsntgywsn ytncaymgnw sngcncayaa ygcnaacncay	300
gcnacntaya cntgycayat ggaygtntty cayttypatgg cngaygayat httywsngtn	360
aayathacng aycarwsngg naaytaywsn cargartgyg gnwsntyyt nytnngar	420
wsnmgnncart ayaayathws ntggmgnwsn gaytaygarg ayccngcntt ytayatgytn	480
aarggnaary tncartayga rytnccartay mgnaaymgng gngayccntg ggcngtnwsn	540
ccnmgnmgna arytnathws ngtngaywsn mgnwsngtnw snytnyncc nytngartty	600
mgnaargayw snwsntayga rytnccartay mgngcnggnc cnatgccngg nwsnwsntay	660
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<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> WXXW motif

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<223> Xaa = Any Amino Acid

<400> 67

Trp Xaa Xaa Trp

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<210> 68

<211> 741

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)...(741)

<400> 68

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5

10

15

ctc ccc act gac cct cca ggc tgg ggc tgc ccc gac ctc gtc tgc tac	96
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Leu	Pro	Thr	Asp	Pro	Pro	Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	
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acc	gat	tac	ctc	cag	acg	gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	144
Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	
				35				40					45			
cac	ccc	agc	acg	ctc	acc	ctt	acc	tgg	ata	ctt	tct	aat	aat	act	ggg	192
His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser	Asn	Asn	Thr	Gly	
				50				55					60			
tgc	tat	atc	aag	gac	aga	aca	ctg	gac	ctc	agg	caa	gac	cag	tat	gaa	240
Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln	Asp	Gln	Tyr	Glu	
				65				70					75			80
gag	ctg	aag	gac	gag	gcc	acc	tcc	tgc	agc	ctc	cac	agg	tgc	gcc	cac	288
Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His	
				85				90					95			
aat	gcc	acg	cat	gcc	acc	tac	acc	tgc	cac	atg	gat	gta	ttc	cac	ttc	336
Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp	Val	Phe	His	Phe	
				100				105					110			
atg	gcc	gac	gac	att	ttc	agt	gtc	aac	atc	aca	gac	cag	tct	ggc	aac	384
Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	
				115				120					125			
tac	tcc	cag	gag	tgt	ggc	agc	ttt	ctc	ctg	gct	gag	agc	aga	cag	tat	432
Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu	Ser	Arg	Gln	Tyr	
				130				135					140			
aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac	cct	gcc	ttc	tac	atg	ctg	480
Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	Pro	Ala	Phe	Tyr	Met	Leu	
				145				150					155			160
aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	tac	agg	aac	cgg	gga	gac	ccc	528
Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Arg	Gly	Asp	Pro	
				165				170					175			
tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	atc	tca	gtg	gac	tca	aga	agt	576
Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile	Ser	Val	Asp	Ser	Arg	Ser	
				180				185					190			

gtc tcc ctc ctc ccc ctg gag ttc cgc aaa gac tcg agc tat gag ctg 624
 Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu
 195 200 205

 cag gtg cg gca ggg ccc atg cct ggc tcc tcc tac cag ggg acc tgg 672
 Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp
 210 215 220

 agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca gag gag tta 720
 Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu
 225 230 235 240

 aag gaa ggc tgg aac cct cac 741
 Lys Glu Gly Trp Asn Pro His
 245

 <210> 69
 <211> 247
 <212> PRT
 <213> Homo sapiens

 <400> 69
 Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro Thr Lys Ala Ser
 1 5 10 15
 Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr
 20 25 30
 Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu
 35 40 45
 His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser Asn Asn Thr Gly
 50 55 60
 Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln Asp Gln Tyr Glu
 65 70 75 80
 Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His
 85 90 95
 Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe
 100 105 110
 Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn
 115 120 125
 Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Arg Gln Tyr
 130 135 140
 Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu
 145 150 155 160

<210> 70
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Domain linker motif; PAPP motif

<400> 70

Pro Ala Pro Pro
1

<210> 71
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Representative variant soluble receptor with
domain linker

<221> VARIANT
<222> (1)...(261)
<223> Xaa = Any Amino Acid

<400> 71

Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro Thr Lys Ala Ser
1 5 10 15

Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr
 20 25 30

Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu
 35 40 45

His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser Asn Asn Thr Gly
 50 55 60

Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln Asp Gln Tyr Glu
 65 70 75 80

Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His
 85 90 95

Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe
 100 105 110

Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn
 115 120 125

Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Xaa Xaa Pro
 130 135 140

Ala Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Gln Tyr Asn Ile
 145 150 155 160

Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly
 165 170 175

Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro Trp Ala
 180 185 190

Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser
 195 200 205

Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val
 210 215 220

Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu
 225 230 235 240

Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu
 245 250 255

Gly Trp Asn Pro His
 260

<210> 72

<211> 1461

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse zalpha1I extracellular domain murine
immunoglobulin gamma 2a heavy chain Fc region
fusion protein (zalpha1Im-mG2a) Polynucleotide

<221> CDS			
<222> (1)...(1461)			
<400> 72			
atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc			48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Cys Gly			
1	5	10	15
gcc gtc ttc gtt tcg ctc agc cag aaa atc cat gcc gag ttg aga cgc			96
Ala Val Phe Val Ser Leu Ser Gln Lys Ile His Ala Glu Leu Arg Arg			
20	25	30	
ttc cg ^g aga tgc ctg gac ctc act tgc tac act gac tac ctc tgg acc			144
Phe Arg Arg Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr			
35	40	45	
atc acc tgt gtc ctg gag aca cg ^g agc ccc aac ccc agc ata ctc agt			192
Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser			
50	55	60	
ctc acc tgg caa gat gaa tat gag gaa ctt cag gac caa gag acc ttc			240
Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe			
65	70	75	80
tgc agc cta cac agg tct ggc cac aac acc aca cat ata tgg tac acg			288
Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr			
85	90	95	
tgc cat atg cgc ttg tct caa ttc ctg tcc gat gaa gtt ttc att gtc			336
Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val			
100	105	110	
aat gtg acg gac cag tct ggc aac aac tcc caa gag tgt ggc agc ttt			384
Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe			
115	120	125	
gtc ctg gct gag agc atc aaa cca gct ccc ttg aac gtg act gtg			432
Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val			
130	135	140	
gcc ttc tca gga cgc tat gat atc tcc tgg gac tca gct tat gac gaa			480

Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu			
145	150	155	160
ccc tcc aac tac gtg ctg agg ggc aag cta caa tat gag ctg cag tat			528
Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr			
165	170	175	
cg ^g aac ctc aga gac ccc tat gct gtg agg cc ^g gtg acc aag ctg atc			576
Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile			
180	185	190	
tca gtg gac tca aga aac gtc tct ctt ctc cct gaa gag ttc cac aaa			624
Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys			
195	200	205	
gat tct agc tac cag ctg cag gtg cg ^g gca gc ^g cct cag cca gg ^c act			672
Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala Ala Pro Gln Pro Gly Thr			
210	215	220	
tca ttc agg ggg acc tgg agt gag tgg agt gac ccc gtc atc ttt cag			720
Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln			
225	230	235	240
acc cag gct ggg gag ccc gag gca gg ^c tgg gac cct cac gag ccc aga			768
Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Glu Pro Arg			
245	250	255	
tct ccc aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac			816
Ser Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn			
260	265	270	
ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat			864
Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp			
275	280	285	
gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat			912
Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp			
290	295	300	
gtg agc gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac			960
Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn			
305	310	315	320

gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat tac aac Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn 325	330	335	1008
agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp 340	345	350	1056
atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro 355	360	365	1104
gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala 370	375	380	1152
cca cag gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys 385	390	395	400
cag gtc act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile 405	410	415	1248
tac gtg gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn 420	425	430	1296
act gaa cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys 435	440	445	1344
ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys 450	455	460	1392
tca gtg gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe 465	470	475	480
tcc cgg act ccg ggt aaa taa			1461

Ser Arg Thr Pro Gly Lys *
485

<210> 73
<211> 486
<212> PRT
<213> Artificial Sequence

<400> 73
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Leu Ser Gln Lys Ile His Ala Glu Leu Arg Arg
 20 25 30
 Phe Arg Arg Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr
 35 40 45
 Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser
 50 55 60
 Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe
 65 70 75 80
 Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr
 85 90 95
 Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val
 100 105 110
 Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe
 115 120 125
 Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val
 130 135 140
 Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu
 145 150 155 160
 Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 165 170 175
 Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile
 180 185 190
 Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys
 195 200 205
 Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala Ala Pro Gln Pro Gly Thr
 210 215 220
 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 225 230 235 240
 Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Glu Pro Arg
 245 250 255

Ser Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn
 260 265 270
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp
 275 280 285
 Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp
 290 295 300
 Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn
 305 310 315 320
 Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
 325 330 335
 Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
 340 345 350
 Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
 355 360 365
 Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala
 370 375 380
 Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys
 385 390 395 400
 Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile
 405 410 415
 Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn
 420 425 430
 Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys
 435 440 445
 Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys
 450 455 460
 Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe
 465 470 475 480
 Ser Arg Thr Pro Gly Lys
 485

<210> 74

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC26644

<400> 74

ggggtcgacg gccggccacc atg

<210> 75 <211> 35 <212> DNA <213> Artificial Sequence	
<220> <223> Oligonucleotide primer ZC26641	
<400> 75 caagttaggtt ccaggcatctt ccggaaacgtt cttaa	35
<210> 76 <211> 35 <212> DNA <213> Artificial Sequence	
<220> <223> Oligonucleotide primer ZC26642	
<400> 76 ttgagacgtt tccggagatgtt cctggacacctc acttg	35
<210> 77 <211> 36 <212> DNA <213> Artificial Sequence	
<220> <223> Oligonucleotide primer ZC26662	
<400> 77 tgtgggagatgtt ctgggctcggtt gagggtccca gctgc	36
<210> 78 <211> 30 <212> DNA <213> Artificial Sequence	
<220> <223> Oligonucleotide primer ZC26643	
<400> 78 gagcccagatctt ccacaaat caagccctgtt	30

<210> 79
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26645

<400> 79
 aaacgcggcc gcggatccgg c 21

<210> 80
 <211> 35
 <212> PRT
 <213> Homo sapeins

<400> 80
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30
 Phe Arg Arg
 35

<210> 81
 <211> 966
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(966)

<400> 81
 ggg ggc ggg ggc gcc gcg cct acg gaa act cag cca cct gtg aca aat 48
 Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
 1 5 10 15

ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata tgg aca tgg aat 96
 Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
 20 25 30

cca ccc gag gga gcc agc tca aat tgt agt cta tgg tat ttt agt cat			144
Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His			
35	40	45	
ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa act cgt cgt tca			192
Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser			
50	55	60	
ata gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag			240
Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln			
65	70	75	80
tgt agc acc aat gag agt gag aag cct agc att ttg gtt gaa aaa tgc			288
Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys			
85	90	95	
atc tca ccc cca gaa ggt gat cct gag tct gct gtg act gag ctt caa			336
Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln			
100	105	110	
tgc att tgg cac aac ctg agc tac atg aag tgt tct tgg ctc cct gga			384
Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly			
115	120	125	
agg aat acc agt ccc gac act aac tat act ctc tac tat tgg cac aga			432
Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg			
130	135	140	
agc ctg gaa aaa att cat caa tgt gaa aac atc ttt aga gaa ggc caa			480
Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln			
145	150	155	160
tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag gat tcc agt ttt			528
Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe			
165	170	175	
gaa caa cac agt gtc caa ata atg gtc aag gat aat gca gga aaa att			576
Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile			
180	185	190	
aaa cca tcc ttc aat ata gtg cct tta act tcc cgt gtg aaa cct gat			624
Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp			
195	200	205	

cct cca cat att aaa aac ctc tcc cac aat gat gac cta tat gtg			672	
Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val				
210	215	220		
caa tgg gag aat cca cag aat ttt att agc aga tgc cta ttt tat gaa			720	
Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu				
225	230	235	240	
gta gaa gtc aat aac agc caa act gag aca cat aat gtt ttc tac gtc			768	
Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val				
245	250	255		
caa gag gct aaa tgt gag aat cca gaa ttt gag aga aat gtg gag aat			816	
Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn				
260	265	270		
aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat act ttg aac aca			864	
Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr				
275	280	285		
gtc aga ata aga gtc aaa aca aat aag tta tgc tat gag gat gac aaa			912	
Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys				
290	295	300		
ctc tgg agt aat tgg agc caa gaa atg agt ata ggt aag aag cgc aat			960	
Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn				
305	310	315	320	
tcc aca			966	
Ser Thr				
<210> 82				
<211> 322				
<212> PRT				
<213> Homo sapiens				
<400> 82				
Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn				
1	5	10	15	
Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn				
20	25	30		

Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His
 35 40 45
 Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser
 50 55 60
 Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln
 65 70 75 80
 Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys
 85 90 95
 Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln
 100 105 110
 Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly
 115 120 125
 Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg
 130 135 140
 Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln
 145 150 155 160
 Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe
 165 170 175
 Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile
 180 185 190
 Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp
 195 200 205
 Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val
 210 215 220
 Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu
 225 230 235 240
 Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val
 245 250 255
 Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
 260 265 270
 Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
 275 280 285
 Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
 290 295 300
 Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
 305 310 315 320
 Ser Thr

<210> 83

<211> 951

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(951)

<400> 83

gac acc gag ata aaa gtt aac cct cct cag gat ttt gag ata gtg gat				48
Asp Thr Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp				
1	5	10	15	
ccc gga tac tta ggt tat ctc tat ttg caa tgg caa ccc cca ctg tct				96
Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser				
20	25	30		
ctg gat cat ttt aag gaa tgc aca gtg gaa tat gaa cta aaa tac cga				144
Leu Asp His Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg				
35	40	45		
aac att ggt agt gaa aca tgg aag acc atc att act aag aat cta cat				192
Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His				
50	55	60		
tac aaa gat ggg ttt gat ctt aac aag ggc att gaa gcg aag ata cac				240
Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His				
65	70	75	80	
acg ctt tta cca tgg caa tgc aca aat gga tca gaa gtt caa agt tcc				288
Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser				
85	90	95		
tgg gca gaa act act tat tgg ata tca cca caa gga att cca gaa act				336
Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr				
100	105	110		
aaa gtt cag gat atg gat tgc gta tat tac aat tgg caa tat tta ctc				384
Lys Val Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu				
115	120	125		
tgt tct tgg aaa cct ggc ata ggt gta ctt ctt gat acc aat tac aac				432
Cys Ser Trp Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn				
130	135	140		
ttg ttt tac tgg tat gag ggc ttg gat cat gca tta cag tgt gtt gat				480

Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ala Leu Gln Cys Val Asp				
145	150	155	160	
tac atc aag gct gat gga caa aat ata gga tgc aga ttt ccc tat ttg				528
Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu				
165	170	175		
gag gca tca gac tat aaa gat ttc tat att tgt gtt aat gga tca tca				576
Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser				
180	185	190		
gag aac aag cct atc aga tcc agt tat ttc act ttt cag ctt caa aat				624
Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn				
195	200	205		
ata gtt aaa cct ttg ccg cca gtc tat ctt act ttt act cgg gag agt				672
Ile Val Lys Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser				
210	215	220		
tca tgt gaa att aag ctg aaa tgg agc ata cct ttg gga cct att cca				720
Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro				
225	230	235	240	
gca agg tgt ttt gat tat gaa att gag atc aga gaa gat gat act acc				768
Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr				
245	250	255		
ttg gtg act gct aca gtt gaa aat gaa aca tac acc ttg aaa aca aca				816
Leu Val Thr Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr				
260	265	270		
aat gaa acc cga caa tta tgc ttt gta gta aga agc aaa gtg aat att				864
Asn Glu Thr Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile				
275	280	285		
tat tgc tca gat gac gga att tgg agt gag tgg agt gat aaa caa tgc				912
Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys				
290	295	300		
tgg gaa ggt gaa gac cta tcg aag aaa act ttg cta cgt				951
Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg				
305	310	315		

<210> 84
<211> 317
<212> PRT
<213> Homo sapiens

<400> 84
Asp Thr Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp
1 5 10 15
Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser
20 25 30
Leu Asp His Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg
35 40 45
Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His
50 55 60
Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His
65 70 75 80
Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser
85 90 95
Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr
100 105 110
Lys Val Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu
115 120 125
Cys Ser Trp Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn
130 135 140
Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ala Leu Gln Cys Val Asp
145 150 155 160
Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu
165 170 175
Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser
180 185 190
Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn
195 200 205
Ile Val Lys Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser
210 215 220
Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro
225 230 235 240
Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr
245 250 255
Leu Val Thr Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr
260 265 270
Asn Glu Thr Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile
275 280 285

Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys
 290 295 300

Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg
 305 310 315

<210> 85

<211> 519

<212> DNA

<213> Homo sapeins

<220>

<221> CDS

<222> (1)...(519)

<400> 85

atc acg tgc cct ccc ccc atg tcc gtg gaa cac gca gac atc tgg gtc	48
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val	
1 5 10 15	

aag agc tac agc ttg tac tcc agg gag cggt tac att tgt aac tct ggt	96
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly	
20 25 30	

ttc aag cgt aaa gcc ggc acg tcc agc ctg acg gag tgc gtg ttg aac	144
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn	
35 40 45	

aag gcc acg aat gtc gcc cac tgg aca acc ccc agt ctc aaa tgc att	192
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile	
50 55 60	

aga gac cct gcc ctg gtt cac caa agg cca gcg cca ccc tcc aca gta	240
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val	
65 70 75 80	

acg acg gca ggg gtg acc cca cag cca gag agc ctc tcc cct tct gga	288
Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly	
85 90 95	

aaa gag ccc gca gct tca tct ccc agc tca aac aac aca gcg gcc aca	336
Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr	
100 105 110	

aca gca gct att gtc ccg ggc tcc cag ctg atg cct tca aaa tca cct	384		
Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro			
115	120	125	
tcc aca gga acc aca gag ata agc agt cat gag tcc tcc cac ggc acc	432		
Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr			
130	135	140	
ccc tct cag aca aca gcc aag aac tgg gaa ctc aca gca tcc gcc tcc	480		
Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser			
145	150	155	160
cac cag ccg cca ggt gtg tat cca cag ggc cac agc gac	519		
His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp			
165	170		
 <210> 86			
<211> 173			
<212> PRT			
<213> Homo sapeins			
 <400> 86			
Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val			
1	5	10	15
Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly			
20	25	30	
Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn			
35	40	45	
Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile			
50	55	60	
Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val			
65	70	75	80
Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly			
85	90	95	
Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr			
100	105	110	
Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro			
115	120	125	
Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr			
130	135	140	
Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser			
145	150	155	160

76

His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp
165 170